OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/904,568

DATE: 07/26/2001
TIME: 18:43:12

Input Set : A:\1272591.app
Output Set: N:\CRF3\07262001\I904568.raw

ENTERED

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 3 <110> APPLICANT: TREMBLAY, Johanne
 4        HAMET, Pavel
 5        LEWANCZUK, Richard
 6        GOSSARD, Francis
 8 <120> TITLE OF INVENTION: A Novel Hypertension Related Calcium Regulated Gene
 9        (HCaRG)
11 <130> FILE REFERENCE: 12725.9
13 <140> CURRENT APPLICATION NUMBER: US/09/904,568
14 <141> CURRENT FILING DATE: 2001-07-16
16 <160> NUMBER OF SEQ ID NOS: 4
18 <170> SOFTWARE: PatentIn Ver. 2.1
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21 <211> LENGTH: 1100
22 <212> TYPE: DNA
23 <213> ORGANISM: Rattus rattus
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34 gggaagaaag g atg tct gct ttg ggg gct gca gct cca tac ttg cac cat 170
35              Met Ser Ala Leu Gly Ala Ala Ala Pro Tyr Leu His His
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38 ccc gct gac agt cac agt ggc cgg gtc agt ttc ctg ggt tcc cag ccc 218
39 Pro Ala Asp Ser His Ser Gly Arg Val Ser Phe Leu Gly Ser Gln Pro
40  15                  20                  25
42 tct cca gaa gtg acg gcc gtg gct cag ctc ttg aag gac tta gac agg 266
43 Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu Lys Asp Leu Asp Arg
44  30                  35                  40                  45
46 agc acc ttc aga aag ttg ttg aaa ctt gta gtc ggg gcc ctg cat ggg 314
47 Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His Gly
48                      50                  55                  60
50 aaa gac tgc aga gaa gct gtg gag caa ctt ggt gcc agc gcc aac ctg 362
51 Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu
52              65                  70                  75
54 tca gaa gag cgt ctg gcc gtc ctg ctg gcg ggc aca cac acc ctg ctc 410
55 Ser Glu Glu Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu
56          80                  85                  90
58 cag cag gct ctc cgg ctg ccc cct gct agt cta aag cca gat gcc ttc 458
59 Gln Gln Ala Leu Arg Leu Pro Pro Ala Ser Leu Lys Pro Asp Ala Phe
60      95                 100                 105
62 cag gaa gag ctc cag gaa ctt ggc att cct cag gat cta att gga gat 506
63 Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln Asp Leu Ile Gly Asp
64 110                 115                 120                 125
66 ttg gcc agt ttg gca ttt ggg agt caa cgc cct ctt ctc gac tct gta 554
67 Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val
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68                    130
70 gcc caa cag cag gga tcc tcg ctg cct cac gtg tct tac ttc cgg tgg   602
71 Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp
72                    145                   150                   155
74 cgg gtg gac gtg gcc atc tca acc agc gct cag tcc cgc tcc ctg caa   650
75 Arg Val Asp Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln
76          160                           165                   170
78 ccg agt gtt ctc atg cag ctg aag ctc aca gat gga tct gca cac cgc   698
79 Pro Ser Val Leu Met Gln Leu Lys Leu Thr Asp Gly Ser Ala His Arg
80      175                           180                   185
82 ttc gag gtg ccc ata gcc aaa ttt cag gag ctg cgg tac agt gta gcc   746
83 Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu Arg Tyr Ser Val Ala
84 190                           195                   200               205
86 ttg gtc ctt aag gag atg gca gaa ctg gag aag aag tgt gag cgc aaa   794
87 Leu Val Leu Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg Lys
88                    210                   215                   220
90 ctg cag gac tgactgaacc ctggtactgt gggtgctgaa gctggtacca            843
91 Leu Gln Asp
93 gaacacagcc ccccactggt gatgagccca actccattga ggtcctgcat gtgagaacgt 903
95 attttaagtg aaaagacagc gggactttca ggttttgttt tatgagtcaa cagctgggca 963
97 gggtggcaca gtttataatc tcagcccttg gaagtctgag gctggagaat gggaagtgta 1023
99 agctgggcct ggctttcata gtgaggctca gtgtcgaatt aaagaggtaa agcaactatt 1083
101 aaaaaaaaaa aaaaaaa                                                 1100
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105 <211> LENGTH: 224
106 <212> TYPE: PRT
107 <213> ORGANISM: Rattus rattus
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116 Val Thr Ala Val Ala Gln Leu Leu Lys Asp Leu Asp Arg Ser Thr Phe
117           35                  40                  45
119 Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His Gly Lys Asp Cys
120      50                  55                  60
122 Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu
123 65                  70                  75                  80
125 Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala
126                85                  90                  95
128 Leu Arg Leu Pro Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu
129           100                 105                 110
131 Leu Gln Glu Leu Gly Ile Pro Gln Asp Leu Ile Gly Asp Leu Ala Ser
132      115                 120                 125
134 Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val Ala Gln Gln
135      130                 135                 140
137 Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp
138 145                 150                 155                 160
140 Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val
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141                  165              Ser Ala His Arg Phe Glu Val
143 Leu Met Gln Leu Lys Leu Thr Asp Gly            185          190
144            180            Phe Gln Glu Leu Arg Tyr Ser Val Ala Leu Val Leu
146 Pro Ile Ala Lys                   200                  205
147      195                   Glu Lys Lys Cys Glu Arg Lys Leu Gln Asp
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161 <222> LOCATION: (295)..(966)
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168 gtccacacgg gacagggacg cccgctcggc tccgctccgc gctgatcctc aaggtctcgc 180
170 ggtttccccg ccgcccaccc ggacgccgac gaaagccagc gagctcctca gcctcaggca 240
172 tctgcatctg ggaccgacct cctgggctgg ctgatcaaag aggaagcagc agca atg 297
                                                                  Met
                                                                   1
173
174
176 tct gct gtg ggg gct gca act cca tac ctg cat cat cct ggt gat agt 345
177 Ser Ala Val Gly Ala Ala Thr Pro Tyr Leu His His Pro Gly Asp Ser
178              5                   10                  15
180 cac agt ggc cga gtg agt ttc ttg ggg gcc cag ctt cct cca gag gtg 393
181 His Ser Gly Arg Val Ser Phe Leu Gly Ala Gln Leu Pro Pro Glu Val
182      20                  25                  30
184 gca gca atg gcc cgg cta cta ggg gac cta gac agg agc acg ttc aga 441
185 Ala Ala Met Ala Arg Leu Leu Gly Asp Leu Asp Arg Ser Thr Phe Arg
186      35                  40                  45
188 aag ttg ctg aag ttt gtg gtc agc agc ctg cag ggg gag gac tgc cga 489
189 Lys Leu Leu Lys Phe Val Val Ser Ser Leu Gln Gly Glu Asp Cys Arg
190 50                  55                  60                  65
192 gac ggt gtg cag cgt ctt ggg gtc agc gcc aac ctg ccg gag gag cag 537
193 Asp Gly Val Gln Arg Leu Gly Val Ser Ala Asn Leu Pro Glu Glu Gln
194              70                  75                  80
196 ctg ggt gcc ctg ctg gca ggc atg cac aca ctg ctc cag cag gcc ctc 585
197 Leu Gly Ala Leu Leu Ala Gly Met His Thr Leu Leu Gln Gln Ala Leu
198              85                  90                  95
200 cgt ctg ccc ccc acc agc ctg aag cct gac acc ttc agg gac cag ctc 633
201 Arg Leu Pro Pro Thr Ser Leu Lys Pro Asp Thr Phe Arg Asp Gln Leu
202      100                 105                 110
204 cag gag ctc tgc atc ccc caa gac ctg gtc ggg gac ttg gcc agc gtg 681
205 Gln Glu Leu Cys Ile Pro Gln Asp Leu Val Gly Asp Leu Ala Ser Val
206      115                 120                 125
208 gta ttt ggg agc cag cgg ccc ctc ctt gat tct gtg gcc cag cag cag 729
209 Val Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val Ala Gln Gln Gln
210 130                 135                 140                 145
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216 gca atc tcc acc agt gcc ctg gct cgc tcc ctg cag ccg agc gtc ctg  825
217 Ala Ile Ser Thr Ser Ala Leu Ala Arg Ser Leu Gln Pro Ser Val Leu
218             165                         170             175
220 atg cag ctg aag ctt tca gat ggg tca gca tac cgc ttt gag gtc ccc  873
221 Met Gln Leu Lys Leu Ser Asp Gly Ser Ala Tyr Arg Phe Glu Val Pro
222     180                         185             190
224 aca gcc aag ttc cag gag ctg cgg tac agc gtg gcc ctg gtc cta aag  921
225 Thr Ala Lys Phe Gln Glu Leu Arg Tyr Ser Val Ala Leu Val Leu Lys
226     195                 200                 205
228 gag atg gca gat ctg gag aag agg tgt gag cgc aga ctg cag gac      966
229 Glu Met Ala Asp Leu Glu Lys Arg Cys Glu Arg Arg Leu Gln Asp
230 210                         215                 220
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234 caaagtgcag ctgactcttc ccacgacagc cctggccttc ccatcaggca ggctcttcag 1086
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248 <211> LENGTH: 224
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250 <213> ORGANISM: Homo sapiens
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262 Arg Lys Leu Leu Lys Phe Val Val Ser Ser Leu Gln Gly Glu Asp Cys
263     50                  55                  60
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266 65                  70                  75                  80
268 Gln Leu Gly Ala Leu Leu Ala Gly Met His Thr Leu Leu Gln Gln Ala
269                 85                  90                  95
271 Leu Arg Leu Pro Pro Thr Ser Leu Lys Pro Asp Thr Phe Arg Asp Gln
272             100                 105                 110
274 Leu Gln Glu Leu Cys Ile Pro Gln Asp Leu Val Gly Asp Leu Ala Ser
275         115                 120                 125
277 Val Val Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser Val Ala Gln Gln
278     130                 135                 140
280 Gln Gly Ala Trp Leu Pro His Val Ala Asp Phe Arg Trp Arg Val Asp
281 145                 150                 155                 160
283 Val Ala Ile Ser Thr Ser Ala Leu Ala Arg Ser Leu Gln Pro Ser Val
284                 165                 170                 175
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286 Leu Met Gln Leu Lys Leu Ser Asp Gly Ser Ala Tyr Arg Phe Glu Val
287             180                 185                 190
289 Pro Thr Ala Lys Phe Gln Glu Leu Arg Tyr Ser Val Ala Leu Val Leu
290             195                 200                 205
292 Lys Glu Met Ala Asp Leu Glu Lys Arg Cys Glu Arg Arg Leu Gln Asp
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VERIFICATION SUMMARY
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DATE: 07/26/2001
TIME: 18:43:13

Input Set : A:\1272591.app
Output Set: N:\CRF3\07262001\I904568.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date